REMARKS

Claims 34-49 are currently active.

Claims 32 and 33 have been cancelled. Claims 34, 37 and 38 have been amended. Claims 39-49 have been added.

Antecedent Support

Antecedent support for the amended Claim 34 is found in the specification on page 40, lines 24 through 25. Specifically, the specification refers to the model of the linear equations that include the matrix A.

Antecedent support for the new Claim 39 is found in the specification on page 40, lines 29 through 30. Specifically, error is computed as the least squares deviation between the observed data and the expected model.

Antecedent support for the new Claim 40 is found in the specification on page 40, lines 28 and 29. Specifically, the minimal least square error solution is mathematically equivalent to the maximum likelihood estimate.

Antecedent support for the new Claim 41 is found in the specification on page 40, lines 8 through 10. Specifically, a matrix equation y = Ax is described.

Antecedent support for the new Claim 42 is found in the specification on page 40, lines 8 through 23. Specifically, the individual modeling roles of x, A, and y in the matrix equation are described.

Antecedent support for the new Claim 43 is found in the specification on page 40, lines 24 through 26. Specifically, the deconvolution process and its motivation are provided.

Antecedent support for the new Claim 44 is found in the specification on page 44, lines 3 through 21. Specifically, the determination of alleles from data when pooling DNA from more than one individual is described.

Antecedent support for the new Claim 45 is found in the specification on page 47, lines 23 through 26, and on page 48, lines 20 through 24, and on page 49, lines 16 through 19. Specifically, mechanisms for estimating the stutter pattern matrix A from DNA data are given.

Antecedent support for the new Claim 46 is found in the specification on page 52, lines 14 through 19, and on page 64, line 29 through page 66, line 5. Specifically, approaches for diagnosing genetic disease and assessing genetic risk in individuals are described.

Antecedent support for the new Claim 47 is found in the specification on page 56, lines 17 through page 57, line 17. Specifically, steps are given for constructing genetic maps.

Antecedent support for the new Claim 48 is found in the specification on page 57, line 18 through page 59, line 3. Specifically, localizing genetic traits on a genome map is described.

Antecedent support for the new Claim 49 is found in the specification on page 60, line 29 through page 62, line 2. Specifically, the positional cloning of disease genes is described.

Rejections Maintained

Examiner rejected claims 34 through 38 under the judicially created doctrine of obviousness-type double patenting as being unpatentable over claims from applicant's previously issued patents.

Applicant respectfully submits that these claims, as amended, are patentably distinct from the method steps of these referenced patents. The amended claims make specific reference to the use of a "linear model" representation that is employed when analyzing the signals. No such specific reference is made in the claims of the issued patents.

Applicant therefore respectfully requests that the objections be withdrawn, and the amended claims 34 through 38 be allowed.

Claim Rejections - 35 USC Section 112

Claims 34-38 were rejected under 35 USC 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicant regards as the invention. This was a new ground of rejection necessitated by Applicant's amendments.

In the amended Claim 34, the step claim language was changed to "identify" an allele, rather than to "produce" an allele.

In the amended Claim 37, the nucleic acid sample processing now links a particular individual to the process. That is, now "there is the step of identifying an individual using the allele of the polymorphism in the individual's nucleic acid material."

In the amended claim 38, the word "comprising" to was changed to "comparing".

In the light of these amendments, Applicant respectfully submits that these amended claims are now not indefinite, and do distinctly claim the subject matter which

Applicant regards as the invention. Applicant respectfully requests that these claims, as amended, now be allowed.

In view of the foregoing amendments and remarks, it is respectfully requested that the outstanding rejections and objections to this application be reconsidered and withdrawn, and Claims 34-49, now in this application be allowed.

Respectfully submitted,

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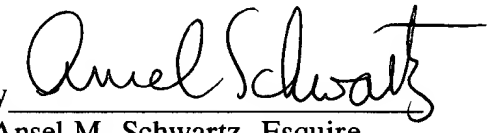
By 

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Version with markings to show changes made to the claims

34. A method of genotyping comprising the steps of:

(a) obtaining nucleic acid material;

(b) amplifying a short tandem repeat polymorphism of the material to produce a signal;

(c) analyzing the signal using a linear model represented in a computing device with a memory; and

(d) [producing] identifying an allele of the polymorphism.

37. A method as described in Claim 34 wherein after the identifying step, there is the step of identifying an individual using the allele of the polymorphism in the individual's nucleic acid material.

38. A method as described in Claim 34 wherein after the identifying step, there is the step of [comprising] comparing the allele with another allele.